



415

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
- (ii) TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
- (iii) NUMBER OF SEQUENCES: 51
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/026,459
 - (B) FILING DATE: 19-FEB-1998
 - (C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/038,118
 - (B) FILING DATE: 20-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hibler, David W.
 - (B) REGISTRATION NUMBER: 41,071
 - (C) REFERENCE/DOCKET NUMBER: UTXC:506
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512/418-3000
 - (B) TELEFAX: 512/474-7577

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	

CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
240 245 250	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
255 260 265 270	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
275 280 285	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
290 295 300	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
305 310 315	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	1008
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
320 325 330	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	1056
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
335 340 345 350	
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	1104
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
355 360 365	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
370 375 380	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
385 390 395	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	1248

Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser		
400						405					410						
ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	1296	
Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe		
415					420					425					430		
GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	1344	
Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr		
				435					440					445			
AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	ATG	CTT	AAA	1392	
Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys		
			450					455					460				
TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	CTT	CTG	AAT	1440	
Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn		
			465				470					475					
GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	GAG	GTT	GTA	1488	
Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val		
	480					485					490						
ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	TCT	GGA	ACA	1536	
Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr		
495					500					505					510		
GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	AAA	GCC	TTT	1584	
Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe		
				515					520					525			
GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	1632	
Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu		
			530					535					540				
ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	1680	
Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met		
			545				550					555					
GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	1728	
Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys		
			560			565				570							
CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT	TGT	1776	
Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys		
575					580					585					590		
CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	GAT	ATG	TAT	1824	
Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr		
				595				600						605			
CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	ACG	CGT	GTA	1872	
Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val		
			610					615						620			

AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
735 740 745 750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
755 760 765	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
770 775 780	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
785 790 795	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
800 805 810	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
815 820 825 830	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG	2544

Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln	
835 840 845	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT	2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser	
850 855 860	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
865 870 875	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG	2688
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu	
880 885 890	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2736
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg	
895 900 905 910	
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA	2784
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu	
915 920 925	
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2840
Glu Lys	
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2960
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3200
TTAATTTAAC ATGAACACCC TTAGAAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA	3260
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3320
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3380
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3440
AACCATATGA TACTATCATA CTA CTGAAAC AGATTTTATA CCTCAGAATG TAAAAAGAACT	3500
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGTC	3555

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10					15		
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25						30		
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
		35						40				45				
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
	50						55				60					
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	
65					70				75						80	
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	
				85					90					95		
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	
			100					105					110			
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	
		115					120					125				
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	
	130					135					140					
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	
145					150					155				160		
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	
			165						170					175		
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	
			180					185					190			
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	
		195					200					205				
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	
	210					215				220						
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	
225					230					235					240	

Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	245	250	255
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	260	265	270
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	275	280	285
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	290	295	300
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
645 650 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
 820 825 830
 Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
 835 840 845
 Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
 850 855 860
 Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
 865 870 875 880
 Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
 885 890 895
 Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
 900 905 910
 Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 915 920 925

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGTC ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile 1 5 10	48
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr 15 20 25 30	96
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu 35 40 45	144
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu 50 55 60	192
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	240

65										70										75										
CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	GAA	GTA	TTA		288													
Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu															
	80						85				90																			
CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	CTA	TGT	GTC		336													
Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val															
	95				100					105					110															
CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	AAA	GAA	CCA		384													
Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro															
				115					120					125																
TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	ACA	CCC	AGG		432													
Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg															
			130					135					140																	
CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	GAA	AAT	GAT		480													
Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp															
		145					150					155																		
ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	AAT	ATA	GAT		528													
Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp															
	160					165					170																			
GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	ATG	AAT	TCT		576													
Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser															
	175				180					185					190															
CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	AAT	CTT	TCT		624													
Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser															
				195					200					205																
AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	GAT	GCA	AGA		672													
Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg															
			210					215					220																	
TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	ATA	GAC	AGT		720													
Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser															
		225					230					235																		
TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	GAA	GAG	GTG		768													
Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val															
	240					245					250																			
AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	AAC	ACT	ATC		816													
Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile															
	255				260					265					270															
CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA		864													
Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu															
				275					280					285																

AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	912
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
290 295 300	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	960
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
305 310 315	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1008
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
320 325 330	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1056
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
335 340 345 350	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1104
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
355 360 365	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1152
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
370 375 380	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1200
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
385 390 395	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1248
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
400 405 410	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1296
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
415 420 425 430	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1344
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
435 440 445	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1392
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
450 455 460	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1440
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
465 470 475	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1488
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
480 485 490	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1536
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	

495		500		505		510	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC							1584
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr							
	515			520		525	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG							1632
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val							
	530			535		540	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG							1680
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu							
	545			550		555	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC							1728
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His							
	560			565		570	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA							1776
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln							
	575			580		585	590
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC							1824
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp							
	595			600		605	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT							1872
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala							
	610			615		620	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT							1920
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Tyr Asp							
	625			630		635	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA							1968
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr							
	640			645		650	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA							2016
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile							
	655			660		665	670
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG							2064
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg							
	675			680		685	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA							2112
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys							
	690			695		700	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA							2160
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg							
	705			710		715	

ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln 720 725 730	2208
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser 735 740 745 750	2256
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp 755 760 765	2304
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu 770 775 780	2352
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg 785 790 795	2400
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu 800 805 810	2448
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG Glu Lys 815	2504
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2564
TTCAGCTCTT TTTGTGGATA TAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2624
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2684
TTTAAAAAGT TGTCAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2744
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	2804
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	2864
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA	2924
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	2984
ATTAGAAAAA AATTACTAAT TTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3044
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3104
AACCATATGA TACTATCATA CTA CTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT	3164
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3218

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val
1				5					10					15	
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val
			20					25					30		
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala
		35					40					45			
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln
	50					55					60				
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys
	65				70					75				80	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met
			85						90					95	
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp
			100					105					110		
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys
		115					120					125			
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly
	130					135					140				
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg
145				150					155					160	
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val
			165					170						175	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly
		180					185						190		
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg
		195				200						205			
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe
	210					215					220				
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu
225					230					235					240

Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	245	250	255	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	260	265	270	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	275	280	285	
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	290	295	300	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	305	310	315	320
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	325	330	335	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	340	345	350	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	355	360	365	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	370	375	380	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	385	390	395	400
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	405	410	415	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	420	425	430	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	435	440	445	
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	450	455	460	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	465	470	475	480
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	485	490	495	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	500	505	510	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	515	520	525	

Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	530	535	540
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	545	550	555
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	565	570	575
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	580	585	590
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	595	600	605
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	610	615	620
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	625	630	635
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	645	650	655
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	660	665	670
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	675	680	685
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	690	695	700
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	705	710	715
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	725	730	735
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	740	745	750
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	755	760	765
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	770	775	780
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	785	790	795
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys	805	810	815

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CTCGAGCAAT GGGCGTGATA GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT      60
GACGTCAATG GGAGTTTGTT TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC      120
AACTCCGCCC CATTGACGCA AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC      180
AGAGCTCGTT TAGTGAACCG TCAGATCGCC TGGAGACGCC ATCCACGCTG TTTTGACCTC      240
CATAGAAGAC ACCGGGACCG ATCCAGCCTC CGCGGCCGCG AATTC                      285
```

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
CCGCTCGAGC AATGGGCGTG GATAGCGG                                         28
```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
CCGCTCGAGC ACCAAAATCA ACGGGA                                           26
```

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCTCGAGC AACTCCGCCC CATTGAC

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGACATATG AATTCGCGGC C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGAATTCG CTGTCTGCC

19

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTAGATG CAGTTGGACC TGGGAG

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTG CCGCCATGTC GTTCACTTTT AC

32

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCCAAGAGA ATTCATAAAA GG

22

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAAGCTTG CCGCCATGGA GCAGGACAGC GGCCCGGAC

39

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCAAGCTTG CCGCCATGGA TTTTACTGCA TTATGTCAG

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCAAGCTTG CCGCCATGGA GAAAGTTTCA TCTTGTGAT

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAAGCTTG CCGCCATGCT GTGGGGAATC TGTATCTTT

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCAAGCTTG CCGCCATGTC AAGACTGTTG AAGAAG

36

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCCTGAGG ACCTAGATGA GATGTCGTTC

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGTTAACC CTAGATGAGA TGTCGTTTAC T

31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCAAGCTTG CCGTCATGCC GCCCAAACC CCCC GA

36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCACCTAGG TCAACTGCTG CAAT

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTTGACCTAG GTGATATGTC GTTC

24

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGCCTAGGA TCTACTGAAA TAAATTCTGC A

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCGATATCA ACTGCTGGGT TGTGTCAAAT A

31

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCG TTTTATATGG TTCTTTGAGC AA

32

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 4..5
- (D) OTHER INFORMATION: /note= "R=A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCRCCAUGG

10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 7..2691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCCGTC ATG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG CTT	48
Met Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu	
1 5 10	
GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG AAA	96
Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys	
15 20 25 30	
TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG	144
Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu	
35 40 45	
AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA	192
Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys	
50 55 60	
AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT	240
Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp	
65 70 75	
GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT	288
Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser	
80 85 90	
GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA	336
Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys	
95 100 105 110	
GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT	384
Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe	
115 120 125	
GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA	432
Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr	
130 135 140	
CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA	480
Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu	
145 150 155	
AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA	528
Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln	
160 165 170	
ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT	576
Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu	
175 180 185 190	
GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT	624
Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr	

195										200					205					
AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	ACA	CCC	AGG	CGA	672				
Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg					
210				215				220												
GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	GAA	AAT	GAT	ACA	720				
Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr					
225				230				235												
AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	AAT	ATA	GAT	GAG	768				
Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu					
240				245				250												
GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	ATG	AAT	TCT	CTT	816				
Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu					
255				260				265				270								
GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	AAT	CTT	TCT	AAA	864				
Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys					
275				280				285												
CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	GAT	GCA	AGA	TTA	912				
Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu					
290				295				300												
TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	ATA	GAC	AGT	TTT	960				
Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe					
305				310				315												
GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	GAA	GAG	GTG	AAT	1008				
Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn					
320				325				330												
GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	AAC	ACT	ATC	CAA	1056				
Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln					
335				340				345				350								
CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA	AAT	1104				
Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn					
355				360				365												
CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	AAA	GAA	AGT	ATA	1152				
Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile					
370				375				380												
CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	GCT	1200				
Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala					
385				390				395												
AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	AAA	1248				
Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys					
400				405				410												

CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA	1296
Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser	
415 420 425 430	
GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC	1344
Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp	
435 440 445	
AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG	1392
Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met	
450 455 460	
GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT	1440
Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp	
465 470 475	
TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT	1488
Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp	
480 485 490	
TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA	1536
Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr	
495 500 505 510	
AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA	1584
Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu	
515 520 525	
TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA	1632
Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln	
530 535 540	
TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT	1680
Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro	
545 550 555	
CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT	1728
Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu	
560 565 570	
TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT	1776
Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn	
575 580 585 590	
TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG	1824
Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln	
595 600 605	
AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT	1872
Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr	
610 615 620	
CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT	1920
Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser	

625	630	635	
GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC			1968
Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr			
640	645	650	
CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT			2016
Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile			
655	660	665	670
ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT			2064
Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu			
675	680	685	
AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT			2112
Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val			
690	695	700	
CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT			2160
Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser			
705	710	715	
ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT			2208
Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn			
720	725	730	
ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT			2256
Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro			
735	740	745	750
CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT			2304
His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile			
755	760	765	
CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT			2352
Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile			
770	775	780	
TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC			2400
Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile			
785	790	795	
TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA			2448
Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys			
800	805	810	
ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT			2496
Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala			
815	820	825	830
GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT			2544
Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile			
835	840	845	

GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC	2592
Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser	
850 855 860	
AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG	2640
Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met	
865 870 875	
CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG	2688
Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu	
880 885 890	
AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2741
Lys	
895	
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2801
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2861
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2921
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2981
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3041
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3101
TTAATTTAAC ATGAACACCC TTAGAAAAATG TGTCCATATCT ATCTTCCAAA TGCAATTTGA	3161
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAAATGGAT ATTATTAGAA	3221
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3281
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3341
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT	3401
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3455

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	Phe
1				5				10					15		

Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	Lys	20	25	30
Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	Val	35	40	45
Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	Glu	50	55	60
Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	Met	65	70	75
Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	His	85	90	95
Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	Asp	100	105	110
Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	115	120	125
Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	130	135	140
Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	145	150	155
Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	165	170	175
Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	180	185	190
Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	195	200	205
Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	210	215	220
Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	225	230	235
Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	245	250	255
Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	260	265	270
Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	275	280	285
Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	290	295	300

Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	305	310	315	320
Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	325	330	335	
Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	340	345	350	
Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	355	360	365	
Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	370	375	380	
Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	385	390	395	400
Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	405	410	415	
Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	420	425	430	
Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	435	440	445	
Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	450	455	460	
Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	465	470	475	480
Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	485	490	495	
Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	500	505	510	
Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	515	520	525	
Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	530	535	540	
Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	545	550	555	560
Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	565	570	575	
Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	580	585	590	

Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	595	600	605	
Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	610	615	620	
Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	625	630	635	640
Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	645	650	655	
Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	660	665	670	
Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	675	680	685	
Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	690	695	700	
Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	705	710	715	720
Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	725	730	735	
Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	740	745	750	
Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	755	760	765	
Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	770	775	780	
Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	785	790	795	800
Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	805	810	815	
Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	820	825	830	
Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	835	840	845	
Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	Phe	850	855	860	
Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	Lys	865	870	875	880

Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
885 890 895

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCATC ATG GAT TTT ACT GCA TTA TGT CAG AAA TTA AAG ATA CCA GAT	48
Met Asp Phe Thr Ala Leu Cys Gln Lys Leu Lys Ile Pro Asp	
1 5 10	
CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG AAA GTT TCA TCT GTG	96
His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys Val Ser Ser Val	
15 20 25 30	
GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA AAG GAA CTG TGG GGA	144
Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys Glu Leu Trp Gly	
35 40 45	
ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT GAG ATG TCG TTC ACT	192
Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu Met Ser Phe Thr	
50 55 60	
TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT GTC CAT AAA TTC TTT	240
Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val His Lys Phe Phe	
65 70 75	
AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA GTT GAT AAT GCT ATG	288
Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val Asp Asn Ala Met	
80 85 90	
TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC TTC AGC AAA	336
Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu Phe Ser Lys	
95 100 105 110	
TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC AGC AGT TCG	384
Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro Ser Ser Ser	
115 120 125	
ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG ATC	432
Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp Ile	
130 135 140	

ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT CTG	480
Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp Leu	
145 150 155	
GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT AAA	528
Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile Lys	
160 165 170	
CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT ATA	576
Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val Ile	
175 180 185 190	
CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT	624
Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser	
195 200 205	
GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT	672
Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val	
210 215 220	
CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT	720
Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr	
225 230 235	
TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT	768
Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser	
240 245 250	
AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT	816
Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile	
255 260 265 270	
TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT	864
Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp	
275 280 285	
AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA	912
Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr	
290 295 300	
CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC	960
Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His	
305 310 315	
ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT	1008
Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile	
320 325 330	
TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT	1056
Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe	
335 340 345 350	
AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG	1104

Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	
				355					360					365		
GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	1152
Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	
			370					375					380			
GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	1200
Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	
		385					390					395				
TAT	TAC	CGA	GTA	ATG	GAA	TCC	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	1248
Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	
	400						405				410					
TCC	ATT	CAA	AAT	TTT	AGC	AAA	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	1296
Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	
415					420				425					430		
TCT	TTA	TTG	GCG	TGC	GCT	CTT	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	1344
Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	
			435					440					445			
AGT	ACA	TCT	CAG	AAT	CTT	GAT	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	1392
Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	
			450					455					460			
ATT	CTG	AAT	GTG	CTT	AAT	TTA	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	1440
Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	
		465					470					475				
GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	1488
Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	
	480					485					490					
CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	1536
His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	
495					500					505				510		
TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	1584
Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	
			515						520					525		
GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	1632
Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	
			530					535					540			
CAG	AAT	AAT	CAC	ACT	GCA	GCA	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	1680
Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	
		545					550					555				
CCA	AAG	AAA	AAA	GGT	TCA	ACT	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	1728
Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	
	560					565					570					

GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT	1776
Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser	
575 580 585 590	
ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC	1824
Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu	
595 600 605	
CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA	1872
Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu	
610 615 620	
GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT	1920
Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr	
625 630 635	
GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG	1968
Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met	
640 645 650	
TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT	2016
Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile	
655 660 665 670	
GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA	2064
Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys	
675 680 685	
CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT	2112
Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr	
690 695 700	
AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT	2160
Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala	
705 710 715	
TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC	2208
Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser	
720 725 730	
CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC	2256
Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile	
735 740 745 750	
TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA	2304
Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro	
755 760 765	
ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT	2352
Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly	
770 775 780	
GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA	2400

Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val	
785	790 795
TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT	2448
Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro	
800	805 810
CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA	2496
Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu	
815	820 825 830
GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA	2544
Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys	
	835 840 845
CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG	2592
Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met	
	850 855 860
AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC	2638
Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
	865 870
AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT	2698
ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA	2758
TAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG	2818
TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT TGTAGCAGAT	2878
TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT	2938
GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG	2998
ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC	3058
TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTGA TTGACTGCCC ATTCACCAAA	3118
ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT	3178
TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA	3238
AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA	3298
CTACTGAAAC AGATTTTCATA CCTCAGAAATG TAAAAGAACT TACTGATTAT TTTCTTCATC	3358
CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3392

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 874 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val
1				5					10					15	
Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly
			20					25					30		
Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys
		35					40					45			
Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr
	50					55					60				
Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu
65					70					75				80	
Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg
				85					90					95	
Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu
			100					105					110		
Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser
		115					120					125			
Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe
	130					135					140				
Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile
145				150						155				160	
Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser
			165						170					175	
Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile
			180					185					190		
Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg
		195					200					205			
Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys
	210					215					220				
Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys
225				230						235				240	
Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly
			245						250					255	

Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	260	265	270
Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	275	280	285
Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	290	295	300
Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	305	310	315
Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	325	330	335
Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	340	345	350
Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	355	360	365
Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	370	375	380
Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	385	390	395
Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	405	410	415
Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	420	425	430
Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	435	440	445
Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	450	455	460
Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	465	470	475
Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	485	490	495
Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	500	505	510
Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	515	520	525
Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	530	535	540

Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys
545 550 555 560

Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr
565 570 575

Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser
580 585 590

Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu
595 600 605

Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His
610 615 620

Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu
625 630 635 640

Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly
645 650 655

Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr
660 665 670

Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val
675 680 685

Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser
690 695 700

Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr
705 710 715 720

Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr
725 730 735

Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile
740 745 750

Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro
755 760 765

Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser
770 775 780

Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn
785 790 795 800

Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys
805 810 815

Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp
820 825 830

Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala
835 840 845

Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp
850 855 860

Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
865 870

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCATC ATG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	48
Met Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
1 5 10	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	96
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
15 20 25 30	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384

Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	
				115					120					125		
GAA	GTA	TTA	CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	432
Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	
			130					135					140			
CTA	TGT	GTC	CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	480
Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	
		145					150					155				
AAA	GAA	CCA	TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	528
Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
	160					165				170						
ACA	CCC	AGG	CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	576
Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
175					180					185					190	
GAA	AAT	GAT	ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	624
Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
				195				200					205			
AAT	ATA	GAT	GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	672
Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
			210					215					220			
ATG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	720
Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
		225					230					235				
AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	768
Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
	240					245					250					
GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	816
Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
255					260					265				270		
ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	864
Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
				275					280					285		
GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	912
Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
			290					295					300			
AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	960
Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
		305					310					315				
CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	1008
Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
	320					325					330					

AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1056
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
335 340 345 350	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1104
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
355 360 365	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1152
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
370 375 380	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1200
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
385 390 395	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1248
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
400 405 410	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1296
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
415 420 425 430	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1344
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
435 440 445	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1392
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
450 455 460	
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1440
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
465 470 475	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1488
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
480 485 490	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1536
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
495 500 505 510	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1584
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
515 520 525	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1632
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
530 535 540	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	1680

Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala		
		545					550					555					
TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	1728	
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr		
	560					565					570						
AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	1776	
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu		
575					580				585						590		
CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	1824	
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu		
				595					600					605			
TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	1872	
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His		
			610					615					620				
TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	1920	
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys		
		625					630					635					
AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	1968	
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu		
	640					645					650						
CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2016	
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu		
655					660					665				670			
GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2064	
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg		
				675					680					685			
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2112	
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu		
			690					695					700				
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2160	
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser		
		705					710					715					
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2208	
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser		
	720					725					730						
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2256	
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro		
735					740					745					750		
AGA	TCA	AGA	ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	2304	
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu		
				755				760						765			

AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2352
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
770 775 780	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2400
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
785 790 795	
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2448
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
800 805 810	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2496
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
815 820 825 830	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2544
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
835 840 845	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2599
Asn Lys Glu Glu Lys	
850	
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC	2659
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2779
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3139
AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG	3259
TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3319
TAGT	3323

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	
1				5					10					15		
Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	
			20					25						30		
Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	
			35					40					45			
Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	
			50				55					60				
Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	
			65			70				75					80	
Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	
				85					90						95	
Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	
			100					105					110			
Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	
			115				120					125				
Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	
			130			135					140					
Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	
			145			150				155					160	
Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	
				165					170						175	
Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	
			180					185					190			
Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	
			195				200					205				
Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	
			210			215					220					
Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	
			225			230				235					240	

Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala
245 250 255

Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp
260 265 270

Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu
275 280 285

Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr
290 295 300

Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser
305 310 315 320

Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu
325 330 335

Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys
340 345 350

Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg
355 360 365

Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu
370 375 380

Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu
385 390 395 400

Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val
405 410 415

Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly
420 425 430

Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala
435 440 445

Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn
450 455 460

Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile
465 470 475 480

Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile
485 490 495

Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala
500 505 510

Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met
515 520 525

Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	530	535	540	
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	545	550	555	560
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	565	570	575	
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	580	585	590	
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	595	600	605	
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	610	615	620	
Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	625	630	635	640
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	645	650	655	
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	660	665	670	
Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	675	680	685	
Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	690	695	700	
Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	705	710	715	720
Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	725	730	735	
Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	740	745	750	
Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	755	760	765	
Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	770	775	780	
Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	785	790	795	800
Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	805	810	815	

Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr
820 825 830

Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys
835 840 845

Glu Glu Lys
850

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCATC ATG CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	48
Met Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
1 5 10	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	96
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
15 20 25 30	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	144
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
35 40 45	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	192
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
50 55 60	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	240
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
65 70 75	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	288
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
80 85 90	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	336
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
95 100 105 110	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	384
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	

115										120					125					
CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	AAA	GAA	CCA	432				
Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro					
130					135					140										
TAT	AAA	ACA	GCT	GTT	ATA	CCC	ATT	AAT	GGT	TCA	CCT	CGA	ACA	CCC	AGG	480				
Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg					
145					150					155										
CGA	GGT	CAG	AAC	AGG	AGT	GCA	CGG	ATA	GCA	AAA	CAA	CTA	GAA	AAT	GAT	528				
Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp					
160					165					170										
ACA	AGA	ATT	ATT	GAA	GTT	CTC	TGT	AAA	GAA	CAT	GAA	TGT	AAT	ATA	GAT	576				
Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp					
175					180					185					190					
GAG	GTG	AAA	AAT	GTT	TAT	TTC	AAA	AAT	TTT	ATA	CCT	TTT	ATG	AAT	TCT	624				
Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser					
195					200					205										
CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT	CCA	GAG	GTT	GAA	AAT	CTT	TCT	672				
Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser					
210					215					220										
AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA	AAT	AAA	GAT	CTA	GAT	GCA	AGA	720				
Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg					
225					230					235										
TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT	CAG	ACT	GAT	TCT	ATA	GAC	AGT	768				
Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser					
240					245					250										
TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA	AGT	AAC	CTT	GAT	GAA	GAG	GTG	816				
Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val					
255					260					265					270					
AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	AAC	ACT	ATC	864				
Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile					
275					280					285										
CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA	912				
Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu					
290					295					300										
AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	AAA	GAA	AGT	960				
Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser					
305					310					315										
ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	1008				
Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe					
320					325					330										

GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1056
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
335 340 345 350	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1104
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
355 360 365	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1152
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
370 375 380	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1200
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
385 390 395	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1248
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
400 405 410	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1296
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
415 420 425 430	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1344
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
435 440 445	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1392
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
450 455 460	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1440
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
465 470 475	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1488
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
480 485 490	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1536
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
495 500 505 510	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1584
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
515 520 525	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1632
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
530 535 540	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1680
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	

545					550					555							
TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	CGC	CTT	CTG	1728	
Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu		
560					565					570							
TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	TTC	CAG	CAC	1776	
Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His		
575					580					585					590		
ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	TTG	GAC	CAA	1824	
Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln		
595					600					605							
ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	AAT	ATA	GAC	1872	
Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp		
610					615					620							
CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	CCT	CAT	GCT	1920	
Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala		
625					630					635							
GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	GAG	TAT	GAT	1968	
Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp		
640					645					650							
TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	CTG	AAA	ACA	2016	
Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr		
655					660					665					670		
AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	TCA	CCA	ATA	2064	
Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile		
675					680					685							
CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	CCC	TTA	CGG	2112	
Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg		
690					695					700							
ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	CCA	TAT	AAA	2160	
Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys		
705					710					715							
ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	AGA	TCA	AGA	2208	
Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg		
720					725					730							
ATC	TTA	GTA	TCA	ATT	GGT	GAA	TCA	TTC	GGG	ACT	TCT	GAG	AAG	TTC	CAG	2256	
Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln		
735					740					745					750		
AAA	ATA	AAT	CAG	ATG	GTA	TGT	AAC	AGC	GAC	CGT	GTG	CTC	AAA	AGA	AGT	2304	
Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser		
755					760					765							

GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2352
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
770 775 780	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG	2400
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu	
785 790 795	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2448
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg	
800 805 810	
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA	2496
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu	
815 820 825 830	
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2552
Glu Lys	
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2612
TTCAGCTCTT TTTGTGGATA TAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2672
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2732
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2792
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	2852
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	2912
TTAATTTAAC ATGAACACCC TTAGAAAATG TGCCTATCT ATCTTCCAAA TGCAATTTGA	2972
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3032
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3092
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3152
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT	3212
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3266

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu
1				5					10					15	
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val
			20					25					30		
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val
		35					40					45			
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala
	50					55					60				
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln
65					70					75					80
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys
				85					90					95	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met
			100					105					110		
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp
	115						120					125			
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys
	130					135					140				
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly
145					150					155					160
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg
			165						170					175	
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val
			180					185					190		
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly
	195						200					205			
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg
	210					215					220				
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe
225					230					235					240
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu
				245					250					255	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val
			260					265					270		
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln

275		280		285
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu				
290		295		300
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu				
305		310		315
Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys				
		325		330
Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu				
		340		345
Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu				
		355		360
Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn				
		370		380
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala				
385		390		395
Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu				
		405		410
Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe				
		420		425
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg				
		435		440
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser				
		450		455
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser				
465		470		475
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu				
		485		490
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser				
		500		505
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser				
		515		520
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys				
		530		535
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg				
545		550		555
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu				

565										570					575				
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu				
			580					585					590						
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met				
		595					600					605							
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys				
	610					615					620								
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln				
625					630					635					640				
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile				
				645					650					655					
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile				
			660					665					670						
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His				
		675					680					685							
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro				
	690					695					700								
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser				
705					710					715				720					
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu				
				725					730					735					
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile				
			740					745					750						
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu				
		755					760					765							
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu				
	770					775					780								
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys				
785					790					795					800				
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln				
				805					810					815					
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys				
			820					825					830						

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 7..2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCCGTC ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC	48
Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu	
1 5 10	
TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC	96
Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro	
15 20 25 30	
AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT	144
Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val	
35 40 45	
TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA	192
Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu	
50 55 60	
GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT	240
Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr	
65 70 75	
TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA	288
Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr	
80 85 90	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	336
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
95 100 105 110	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	384
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
115 120 125	
ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA	432
Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys	
130 135 140	
AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT	480
Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu	
145 150 155	
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC	528
Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr	
160 165 170	

GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG	576
Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu	
175 180 185 190	
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA	624
Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr	
195 200 205	
CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT	672
Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile	
210 215 220	
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA	720
Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu	
225 230 235	
ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT	768
Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile	
240 245 250	
TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA	816
Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys	
255 260 265 270	
AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT	864
Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala	
275 280 285	
GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA	912
Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly	
290 295 300	
GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA	960
Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu	
305 310 315	
GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT	1008
Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile	
320 325 330	
TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA	1056
Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr	
335 340 345 350	
TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT	1104
Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser	
355 360 365	
TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC	1152
Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr	
370 375 380	
AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA	1200

Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu		
	385						390					395					
ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	1248	
Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu		
	400					405					410						
GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	1296	
Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys		
	415				420					425					430		
GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT	TGT	CCT	CTT	AAT	1344	
Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn		
				435					440					445			
CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	GAT	ATG	TAT	CTT	TCT	CCT	1392	
Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro		
			450					455					460				
GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	ACG	CGT	GTA	AAT	TCT	ACT	1440	
Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr		
	465						470					475					
GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	TTC	CAG	ACC	CAG	AAG	CCA	1488	
Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro		
	480					485					490						
TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	AAA	AAA	GTG	TAT	CGG	CTA	1536	
Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu		
	495				500					505					510		
GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	CGC	CTT	CTG	TCT	GAG	CAC	1584	
Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His		
				515					520					525			
CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	TTC	CAG	CAC	ACC	CTG	CAG	1632	
Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln		
			530					535					540				
AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	TTG	GAC	CAA	ATT	ATG	ATG	1680	
Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met		
	545						550					555					
TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	AAT	ATA	GAC	CTT	AAA	TTC	1728	
Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe		
	560					565					570						
AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	CCT	CAT	GCT	GTT	CAG	GAG	1776	
Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu		
	575				580				585					590			
ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	GAG	TAT	GAT	TCT	ATT	ATA	1824	
Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile		
				595				600						605			

GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1872
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
610 615 620	
CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT	1920
Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile	
625 630 635	
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA	1968
Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly	
640 645 650	
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA	2016
Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu	
655 660 665 670	
GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA	2064
Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val	
675 680 685	
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT	2112
Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn	
690 695 700	
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA	2160
Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly	
705 710 715	
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA	2208
Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly	
720 725 730	
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT	2256
Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe	
735 740 745 750	
CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG	2304
Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys	
755 760 765	
CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA	2349
Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
770 775 780	
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2409
ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2469
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2529
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2589
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2649

GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG 2709
 CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC 2769
 ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTGA TTGACTGCCC 2829
 ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA 2889
 AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT 2949
 TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA 3009
 TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT TACTGATTAT 3069
 TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT 3113

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	1	5	10	15
Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	20	25	30	
Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	35	40	45	
Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	50	55	60	
Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	65	70	75	80
Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	85	90	95	
Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	100	105	110	
Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	115	120	125	
Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val				

130		135		140
Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr				
145		150		155
Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu				
	165		170	175
Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His				
	180		185	190
Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg				
	195		200	205
Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro				
	210		215	220
His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met				
	225		230	235
Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr				
	245		250	255
Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val				
	260		265	270
Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly				
	275		280	285
Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg				
	290		295	300
Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg				
	305		310	315
Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His				
	325		330	335
Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser				
	340		345	350
Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro				
	355		360	365
Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val				
	370		375	380
Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile				
	385		390	395
Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp				
	405		410	415
Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg				

705	710	715	720
Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp			
	725	730	735
Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln			
	740	745	750
Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys			
	755	760	765
Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys			
	770	775	780

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GTC GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336

Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
115 120 125	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	432
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
130 135 140	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	480
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
145 150 155	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	528
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160 165 170	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	576
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
175 180 185 190	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	624
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
195 200 205	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	672
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
210 215 220	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	720
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
225 230 235	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	768
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
240 245 250	
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	816
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
255 260 265 270	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	864
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
275 280 285	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	912
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
290 295 300	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	960
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
305 310 315	

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1008
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
320 325 330	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1056
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
335 340 345 350	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1104
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
355 360 365	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1152
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
370 375 380	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1200
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
385 390 395	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1248
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
400 405 410	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1296
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
415 420 425 430	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1344
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
435 440 445	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1392
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
450 455 460	
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1440
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
465 470 475	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1488
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
480 485 490	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1536
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
495 500 505 510	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1584
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
515 520 525	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1632

Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr		
			530					535					540				
ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	1680	
Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala		
		545					550					555					
TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	1728	
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr		
	560					565					570						
AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	1776	
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu		
575					580				585						590		
CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	1824	
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu		
			595				600						605				
TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	1872	
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His		
		610					615						620				
TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	1920	
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys		
		625				630						635					
AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	1968	
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu		
	640					645					650						
CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	2016	
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu		
655					660				665					670			
GAG	TAT	GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	2064	
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg		
			675					680					685				
CTG	AAA	ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	2112	
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu		
		690					695						700				
TCA	CCA	ATA	CCT	CAC	ATT	CCT	CGA	AGC	CCT	TAC	AAG	TTT	CCT	AGT	TCA	2160	
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser		
		705					710					715					
CCC	TTA	CGG	ATT	CCT	GGA	GGG	AAC	ATC	TAT	ATT	TCA	CCC	CTG	AAG	AGT	2208	
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser		
	720					725					730						
CCA	TAT	AAA	ATT	TCA	GAA	GGT	CTG	CCA	ACA	CCA	ACA	AAA	ATG	ACT	CCA	2256	
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro		
735					740				745						750		

AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG	2304
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu	
755 760 765	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2352
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
770 775 780	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2400
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
785 790 795	
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2448
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
800 805 810	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2496
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
815 820 825 830	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2544
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
835 840 845	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2599
Asn Lys Glu Lys	
850	
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC	2659
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2779
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTAATTATTG	3139
AATCTGATAT ACTGTGTGCT TGTTTATATA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG	3259
TAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3319
TAGT	3323

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10						15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Val	Asp	
			20					25						30		
Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	
			35					40					45			
Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	
	50						55					60				
Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	
	65					70					75				80	
Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	
				85					90						95	
Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	
			100						105					110		
Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	
		115					120						125			
Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	
		130					135				140					
Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	
	145					150					155				160	
Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	
				165					170						175	
Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	
			180						185					190		
Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	
		195						200					205			
Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	
		210						215							220	

Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu
225 230 235 240

Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala
245 250 255

Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp
260 265 270

Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu
275 280 285

Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr
290 295 300

Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser
305 310 315 320

Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu
325 330 335

Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys
340 345 350

Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg
355 360 365

Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu
370 375 380

Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu
385 390 395 400

Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val
405 410 415

Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly
420 425 430

Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala
435 440 445

Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn
450 455 460

Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile
465 470 475 480

Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile
485 490 495

Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala
500 505 510

Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met
515 520 525

Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg
530 535 540

Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln
545 550 555 560

Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys
565 570 575

Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu
580 585 590

Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln
595 600 605

His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp
610 615 620

Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile
625 630 635 640

Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His
645 650 655

Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr
660 665 670

Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys
675 680 685

Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro
690 695 700

Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu
705 710 715 720

Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr
725 730 735

Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser
740 745 750

Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe
755 760 765

Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg
770 775 780

Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe
785 790 795 800

Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly
805 810 815

Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr
820 825 830

Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys
835 840 845

Glu Glu Lys
850

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTG GTC GAC	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Val Asp	
65 70 75	
CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA	288
Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu	
80 85 90	
ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT	336
Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser	

95	100	105	110	
ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA				384
Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val	115	120	125	
TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT				432
Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr	130	135	140	
TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG				480
Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu	145	150	155	
GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA				528
Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val	160	165	170	
TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT				576
Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys	175	180	185	190
GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA				624
Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu	195	200	205	
CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC				672
Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro	210	215	220	
AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT				720
Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn	225	230	235	
GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA				768
Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile	240	245	250	
GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT				816
Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn	255	260	265	270
TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT				864
Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu	275	280	285	
TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA				912
Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala	290	295	300	
AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC				960
Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp	305	310	315	

AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG	1008
Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu	
320 325 330	
GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT	1056
Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr	
335 340 345 350	
ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA	1104
Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser	
355 360 365	
GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA	1152
Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu	
370 375 380	
AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA	1200
Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys	
385 390 395	
TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA	1248
Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg	
400 405 410	
TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT	1296
Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu	
415 420 425 430	
AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG	1344
Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu	
435 440 445	
AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT	1392
Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val	
450 455 460	
GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA	1440
Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly	
465 470 475	
ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC	1488
Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala	
480 485 490	
TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC	1536
Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn	
495 500 505 510	
TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC	1584
Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile	
515 520 525	
ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT	1632
Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile	

530										535										540										
AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT		1680													
Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala															
545					550					555																				
TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	GAT	ATG		1728													
Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met															
560					565					570																				
TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	ACG	CGT		1776													
Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg															
575					580					585					590															
GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	TTC	CAG		1824													
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln															
595					600					605																				
ACC	CAG	AAG	CCA	TTG	AAA	TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	AAA	AAA		1872													
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys															
610					615					620																				
GTG	TAT	CGG	CTA	GCC	TAT	CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	CGC	CTT		1920													
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu															
625					630					635																				
CTG	TCT	GAG	CAC	CCA	GAA	TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	TTC	CAG		1968													
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln															
640					645					650																				
CAC	ACC	CTG	CAG	AAT	GAG	TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	TTG	GAC		2016													
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp															
655					660					665					670															
CAA	ATT	ATG	ATG	TGT	TCC	ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	AAT	ATA		2064													
Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile															
675					680					685																				
GAC	CTT	AAA	TTC	AAA	ATC	ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	CCT	CAT		2112													
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His															
690					695					700																				
GCT	GTT	CAG	GAG	ACA	TTC	AAA	CGT	GTT	TTG	ATC	AAA	GAA	GAG	GAG	TAT		2160													
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr															
705					710					715																				
GAT	TCT	ATT	ATA	GTA	TTC	TAT	AAC	TCG	GTC	TTC	ATG	CAG	AGA	CTG	AAA		2208													
Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys															
720					725					730																				
ACA	AAT	ATT	TTG	CAG	TAT	GCT	TCC	ACC	AGG	CCC	CCT	ACC	TTG	TCA	CCA		2256													
Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro															
735					740					745					750															

ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu 755 760 765	2304
CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr 770 775 780	2352
AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser 785 790 795	2400
AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe 800 805 810	2448
CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg 815 820 825 830	2496
AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe 835 840 845	2544
GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly 850 855 860	2592
GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr 865 870 875	2640
CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys 880 885 890	2688
GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT Glu Glu Lys 895	2737
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC	2797
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA	2857
TTCTTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2917
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2977
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	3037
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	3097
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA	3157

TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT 3217
 ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG 3277
 AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA 3337
 AGCAAAGTAT AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG 3397
 TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA 3457
 TAGT 3461

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	
1				5					10					15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp
			20					25					30		
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu
		35					40					45			
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu
	50					55					60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Val	Asp	Leu	Asp
	65				70				75					80	
Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser
				85					90					95	
Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys
			100					105					110		
Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe
		115					120					125			
Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr
	130				135						140				
Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu
145					150					155				160	

Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	165	170	175	
Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	180	185	190	
Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	195	200	205	
Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	210	215	220	
Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	225	230	235	240
Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	245	250	255	
Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	260	265	270	
Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	275	280	285	
Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	290	295	300	
Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	305	310	315	320
Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	325	330	335	
Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	340	345	350	
Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	355	360	365	
Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	370	375	380	
Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	385	390	395	400
Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	405	410	415	
Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	420	425	430	
Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	435	440	445	

Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	450	455	460	
Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	465	470	475	480
Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	485	490	495	
Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	500	505	510	
Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	515	520	525	
Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	530	535	540	
Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	545	550	555	560
Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	565	570	575	
Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	580	585	590	
Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	595	600	605	
Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	610	615	620	
Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	625	630	635	640
Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	645	650	655	
Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	660	665	670	
Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	675	680	685	
Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	690	695	700	
Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	705	710	715	720
Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	725	730	735	

Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro
 740 745 750
 His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile
 755 760 765
 Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile
 770 775 780
 Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile
 785 790 795 800
 Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys
 805 810 815
 Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala
 820 825 830
 Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile
 835 840 845
 Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser
 850 855 860
 Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met
 865 870 875 880
 Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu
 885 890 895
 Lys

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	

15	20	25	30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG				144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg				
	35	40	45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG				192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln				
	50	55	60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG				240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp				
	65	70	75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG				288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys				
	80	85	90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA				336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu				
	95	100	105	110
GTC GAA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG				384
Val Glu Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp				
	115	120	125	
ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT				432
Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp				
	130	135	140	
CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT				480
Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile				
	145	150	155	
AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT				528
Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val				
	160	165	170	
ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG				576
Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg				
	175	180	185	190
AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA				624
Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu				
	195	200	205	
GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT				672
Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val				
	210	215	220	
TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA				720
Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr				
	225	230	235	

TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu 240 245 250	768
ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His 255 260 265 270	816
GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg 275 280 285	864
ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro 290 295 300	912
CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met 305 310 315	960
ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr 320 325 330	1008
TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val 335 340 345 350	1056
AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly 355 360 365	1104
CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg 370 375 380	1152
TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg 385 390 395	1200
TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His 400 405 410	1248
ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser 415 420 425 430	1296
AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro 435 440 445	1344
TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val	1392

450										455					460					
ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	1440				
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile					
465					470					475										
AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	1488				
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp					
480					485					490										
CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	1536				
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg					
495					500					505					510					
GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	1584				
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro					
515					520					525										
CTC	CAG	AAT	AAT	CAC	ACT	GCA	GCA	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	1632				
Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg					
530					535					540										
TCT	CCA	AAG	AAA	AAA	GGT	TCA	ACT	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	1680				
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn					
545					550					555										
GCA	GAG	ACA	CAA	GCA	ACC	TCA	GCC	TTC	CAG	ACC	CAG	AAG	CCA	TTG	AAA	1728				
Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys					
560					565					570										
TCT	ACC	TCT	CTT	TCA	CTG	TTT	TAT	AAA	AAA	GTG	TAT	CGG	CTA	GCC	TAT	1776				
Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr					
575					580					585					590					
CTC	CGG	CTA	AAT	ACA	CTT	TGT	GAA	CGC	CTT	CTG	TCT	GAG	CAC	CCA	GAA	1824				
Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu					
595					600					605										
TTA	GAA	CAT	ATC	ATC	TGG	ACC	CTT	TTC	CAG	CAC	ACC	CTG	CAG	AAT	GAG	1872				
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu					
610					615					620										
TAT	GAA	CTC	ATG	AGA	GAC	AGG	CAT	TTG	GAC	CAA	ATT	ATG	ATG	TGT	TCC	1920				
Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser					
625					630					635										
ATG	TAT	GGC	ATA	TGC	AAA	GTG	AAG	AAT	ATA	GAC	CTT	AAA	TTC	AAA	ATC	1968				
Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile					
640					645					650										
ATT	GTA	ACA	GCA	TAC	AAG	GAT	CTT	CCT	CAT	GCT	GTT	CAG	GAG	ACA	TTC	2016				
Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe					
655					660					665					670					

AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC	2064
Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe	
675 680 685	
TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT	2112
Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr	
690 695 700	
GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA	2160
Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg	
705 710 715	
AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC	2208
Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn	
720 725 730	
ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG	2256
Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu	
735 740 745 750	
CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT	2304
Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile	
755 760 765	
GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG	2352
Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met	
770 775 780	
GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC	2400
Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn	
785 790 795	
CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT	2448
Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp	
800 805 810	
GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG	2496
Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln	
815 820 825 830	
AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA	2544
Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys	
835 840 845	
ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC	2593
Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
850 855	
AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT	2653
ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA	2713
TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG	2773

TTATTTATAC AAGATTGAAA ATCTTGTA AATCCTGCCA TTTAAAAAGT TGTCAGCAT	2833
TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT	2893
GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG	2953
ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC	3013
TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTGA TTGACTGCCC ATTCACCAAA	3073
ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT	3133
TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA	3193
AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA	3253
CTACTGAAAC AGATTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC	3313
CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3347

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	1	5	10	15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	65	70	75	80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	85	90	95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Val	Glu	100	105	110	
Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr				

115					120					125					
Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val
130					135					140					
Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu
145					150					155					160
Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro
				165					170					175	
Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala
			180					185					190		
Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu
		195					200					205			
Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe
	210					215					220				
Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn
225					230					235					240
Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr
				245					250					255	
Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys
			260					265					270		
Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro
			275				280					285			
Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr
	290					295					300				
Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu
305					310					315					320
Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn
				325					330					335	
Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp
			340					345					350		
Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly
	355					360						365			
Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr
	370					375					380				
Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser
385					390					395					400
Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser

405										410					415				
Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser				
			420						425						430				
Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile				
		435					440					445							
Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu				
		450				455					460								
Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His				
465					470					475					480				
Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser				
				485					490						495				
Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly				
			500					505					510						
Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln				
		515					520					525							
Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro				
		530				535					540								
Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu				
545					550					555					560				
Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr				
				565					570						575				
Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg				
			580					585					590						
Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu				
		595					600					605							
His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu				
	610					615					620								
Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr				
625					630					635					640				
Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val				
			645						650					655					
Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg				
			660					665					670						
Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn				
		675					680					685							
Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser				

690	695	700
Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro		
705	710	715 720
Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr		
	725	730 735
Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr		
	740	745 750
Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu		
	755	760 765
Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys		
	770	775 780
Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro		
	785	790 795 800
Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala		
	805	810 815
Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu		
	820	825 830
Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn		
	835	840 845
Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys		
	850	855

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	

GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	384
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
115 120 125	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	432
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
130 135 140	
ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA	480
Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys	
145 150 155	
AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT	528
Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu	
160 165 170	
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC	576
Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr	
175 180 185 190	
GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG	624
Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu	
195 200 205	
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA	672
Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr	
210 215 220	
CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT	720
Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile	
225 230 235	
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA	768

Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	
240						245					250					
ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA	AAT	CTG	ATT	816
Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	
255					260					265					270	
TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	AAA	GAA	AGT	ATA	CTG	AAA	864
Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	
				275					280						285	
AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	GCT	AAA	GCT	912
Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	
			290					295					300			
GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	AAA	CTT	GGA	960
Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	
		305						310					315			
GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	ATG	CTT	AAA	TCA	GAA	GAA	1008
Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	
		320					325					330				
GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	CTT	CTG	AAT	GAC	AAC	ATT	1056
Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	
335						340					345				350	
TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	GAG	GTT	GTA	ATG	GCC	ACA	1104
Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	
				355						360					365	
TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	TCT	GGA	ACA	GAT	TTG	TCT	1152
Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	
			370						375					380		
TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	AAA	GCC	TTT	GAT	TTT	TAC	1200
Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	
		385						390					395			
AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	ACA	AGA	GAA	1248
Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	
	400						405					410				
ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	1296
Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	
415						420					425				430	
GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	1344
Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	
				435						440					445	
GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC	CTT	GAA	TCT	GCT	TGT	CCT	CTT	AAT	1392
Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	
			450						455						460	

CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT	1440
Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro	
465 470 475	
GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT	1488
Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr	
480 485 490	
GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA	1536
Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro	
495 500 505 510	
TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA	1584
Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu	
515 520 525	
GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC	1632
Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His	
530 535 540	
CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG	1680
Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln	
545 550 555	
AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG	1728
Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met	
560 565 570	
TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC	1776
Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe	
575 580 585 590	
AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG	1824
Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu	
595 600 605	
ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA	1872
Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile	
610 615 620	
GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1920
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
625 630 635	
CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT	1968
Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile	
640 645 650	
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA	2016
Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly	
655 660 665 670	
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA	2064

Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu	
675 680 685	
GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA	2112
Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val	
690 695 700	
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT	2160
Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn	
705 710 715	
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA	2208
Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly	
720 725 730	
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA	2256
Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly	
735 740 745 750	
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT	2304
Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe	
755 760 765	
CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG	2352
Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys	
770 775 780	
CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA	2397
Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
785 790 795	
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2457
ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2517
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2577
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2637
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2697
GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG	2757
CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC	2817
ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC	2877
ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAAATGGAT ATTATTAGAA ATTAGAAAAA	2937
AATTACTAAT TTTACACATT AGATTTTATT TTAATTTGAT AATCTGATAT ACTGTGTGCT	2997
TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA	3057
TACTATCATA CTAATGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT	3117

TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT

3161

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10						15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25							30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
			35					40					45			
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
			50				55					60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	
	65					70				75					80	
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	
				85						90					95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Ala	Val	
			100						105					110		
Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	
			115					120					125			
Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	
			130				135					140				
Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	
			145			150				155					160	
Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	
				165					170						175	
Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	
			180						185					190		
Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	
			195					200						205		

Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	210	215	220
Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	225	230	235
His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	245	250	255
Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	260	265	270
Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	275	280	285
Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	290	295	300
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	305	310	315
Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	325	330	335
Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	340	345	350
Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	355	360	365
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	370	375	380
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	385	390	395
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	405	410	415
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	420	425	430
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	435	440	445
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	450	455	460
Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	465	470	475
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	485	490	495

Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys		
			500					505					510				
Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr		
		515					520					525					
Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu		
	530					535					540						
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu		
545					550					555					560		
Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser		
				565					570					575			
Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile		
			580					585					590				
Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe		
		595					600					605					
Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe		
	610					615					620						
Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr		
625					630					635					640		
Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg		
				645					650					655			
Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn		
			660					665					670				
Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu		
	675						680					685					
Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile		
	690					695					700						
Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met		
705					710					715					720		
Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn		
				725					730					735			
Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp		
			740					745					750				
Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln		
		755					760					765					
Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys		
	770					775					780						

Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 785 790 795

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	

AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATG GTC GCT GTT ATA CCC ATT AAT GGT TCA	576
Thr Gln Pro Ser Ser Ser Met Val Ala Val Ile Pro Ile Asn Gly Ser	
175 180 185 190	
CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA	624
Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys	
195 200 205	
CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT	672
Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His	
210 215 220	
GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA	720
Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile	
225 230 235	
CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG	768
Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu	
240 245 250	
GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA	816
Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys	
255 260 265 270	
GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT	864
Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr	
275 280 285	
GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC	912
Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn	
290 295 300	
CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT	960
Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr	
305 310 315	
GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT	1008
Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser	
320 325 330	
GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG	1056
Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val	
335 340 345 350	
AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC	1104
Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile	

																355																	360																	365
TTT	AAA	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT																	1152																		
Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile																																			
				370				375				380																																						
GGA	TCA	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG																	1200																		
Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met																																			
				385				390				395																																						
GAA	TCC	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT																	1248																		
Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe																																			
				400				405				410																																						
AGC	AAA	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC																	1296																		
Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys																																			
				415				420				425				430																																		
GCT	CTT	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT																	1344																		
Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn																																			
				435				440				445																																						
CTT	GAT	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT																	1392																		
Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu																																			
				450				455				460																																						
AAT	TTA	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA																	1440																		
Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys																																			
				465				470				475																																						
GCA	GAA	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT																	1488																		
Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys																																			
				480				485				490																																						
GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA																	1536																		
Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu																																			
				495				500				505				510																																		
TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	GAA	GGA	CCA	ACT	GAT	CAC																	1584																		
Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His																																			
				515				520				525																																						
CTT	GAA	TCT	GCT	TGT	CCT	CTT	AAT	CTT	CCT	CTC	CAG	AAT	AAT	CAC	ACT																	1632																		
Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr																																			
				530				535				540																																						
GCA	GCA	GAT	ATG	TAT	CTT	TCT	CCT	GTA	AGA	TCT	CCA	AAG	AAA	AAA	GGT																	1680																		
Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly																																			
				545				550				555																																						
TCA	ACT	ACG	CGT	GTA	AAT	TCT	ACT	GCA	AAT	GCA	GAG	ACA	CAA	GCA	ACC																	1728																		
Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Al																																				

TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG	1776
Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu	
575 580 585 590	
TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT	1824
Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu	
595 600 605	
TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG	1872
Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp	
610 615 620	
ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC	1920
Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp	
625 630 635	
AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA	1968
Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys	
640 645 650	
GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG	2016
Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys	
655 660 665 670	
GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA	2064
Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys	
675 680 685	
GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG	2112
Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met	
690 695 700	
CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT	2160
Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro	
705 710 715	
ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT	2208
Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro	
720 725 730	
AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG	2256
Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu	
735 740 745 750	
AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG	2304
Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met	
755 760 765	
ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT	2352
Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr	
770 775 780	
TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT	2400
Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg	

785	790	795	
GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA			2448
Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys			
800	805	810	
AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA			2496
Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys			
815	820	825	830
CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT			2544
His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr			
	835	840	845
TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT			2592
Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp			
	850	855	860
ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT			2643
Thr Ser Asn Lys Glu Glu Lys			
865			
GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT			2703
TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT			2763
GTTTGGGTGA TTCCTAAGCC ACTTGAAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA			2823
ATCTTGTTGTA AATCCTGCCA TTTAAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA			2883
AATGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG			2943
CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT			3003
TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCATCT			3063
ATCTTCCAAA TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC			3123
AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT			3183
TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT			3243
AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC AGATTTTATA			3303
CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA			3363
GGATTATTGA TAGT			3377

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10						15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25						30		
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
		35					40					45				
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
	50						55					60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	
65					70				75						80	
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	
				85				90						95		
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	
			100					105					110			
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	
		115					120					125				
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	
	130						135				140					
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	
145					150					155					160	
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	
				165					170					175		
Pro	Ser	Ser	Ser	Met	Val	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
				180				185					190			
Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
		195					200					205				
Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
	210					215					220					
Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
225					230					235					240	
Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
				245					250					255		

Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	260	265	270
Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	275	280	285
Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	290	295	300
Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	305	310	315
Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	325	330	335
Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	340	345	350
Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	355	360	365
Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	370	375	380
Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	385	390	395
Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	405	410	415
Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	420	425	430
Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	435	440	445
Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	450	455	460
Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	465	470	475
Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	485	490	495
Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	500	505	510
Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	515	520	525
Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	530	535	540

Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	545	550	555	560
Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	565	570	575	
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	580	585	590	
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	595	600	605	
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	610	615	620	
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	625	630	635	640
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	645	650	655	
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	660	665	670	
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	675	680	685	
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	690	695	700	
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	705	710	715	720
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	725	730	735	
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	740	745	750	
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	755	760	765	
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	770	775	780	
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	785	790	795	800
Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	805	810	815	
Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	820	825	830	

Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
835 840 845

Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
850 855 860

Asn Lys Glu Glu Lys
865

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	

115												120												125												
AGT	GTC	CAT	AAA	TTC	TTT	AAC	TTA	CTA	AAA	GAA	ATT	GAT	ACC	AGT	ACC		432																			
Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr																					
			130						135						140																					
AAA	GTT	GAT	AAT	GCT	ATG	TCA	AGA	CTG	TTG	AAG	AAG	TAT	GAT	GTA	TTG		480																			
Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu																					
			145					150					155																							
TTT	GCA	CTC	TTC	AGC	AAA	TTG	GAA	AGG	ACA	TGT	GAA	CTT	ATA	TAT	TTG		528																			
Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu																					
		160					165				170																									
ACA	CAA	CCC	AGC	AGT	TCG	ATA	TCT	ACT	GAA	ATA	AAT	TCT	GCA	TTG	GTG		576																			
Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val																					
		175				180				185					190																					
CTA	AAA	GTT	TCT	TGG	ATC	ACA	TTT	TTA	TTA	GCT	AAA	GGG	GAA	GTA	TTA		624																			
Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu																					
			195					200						205																						
CAA	ATG	GAA	GAT	GAT	CTG	GTG	ATT	TCA	TTT	CAG	TTA	ATG	CTA	TGT	GTC		672																			
Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val																					
			210					215					220																							
CTT	GAC	TAT	TTT	ATT	AAA	CTC	TCA	CCT	CCC	ATG	TTG	CTC	AAA	GAA	CCA		720																			
Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro																					
		225					230					235																								
TAT	AAA	ACA	GGG	TCG	AAT	TCT	CTT	GGA	CTT	GTA	ACA	TCT	AAT	GGA	CTT		768																			
Tyr	Lys	Thr	Gly	Ser	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu																					
		240					245				250																									
CCA	GAG	GTT	GAA	AAT	CTT	TCT	AAA	CGA	TAC	GAA	GAA	ATT	TAT	CTT	AAA		816																			
Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys																					
		255				260				265					270																					
AAT	AAA	GAT	CTA	GAT	GCA	AGA	TTA	TTT	TTG	GAT	CAT	GAT	AAA	ACT	CTT		864																			
Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu																					
			275						280					285																						
CAG	ACT	GAT	TCT	ATA	GAC	AGT	TTT	GAA	ACA	CAG	AGA	ACA	CCA	CGA	AAA		912																			
Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys																					
			290					295					300																							
AGT	AAC	CTT	GAT	GAA	GAG	GTG	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT		960																			
Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val																					
		305					310					315																								
AGG	ACT	GTT	ATG	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA		1008																			
Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser																					
		320					325					330																								

GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC	1056
Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys	
335 340 345 350	
ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA	1104
Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly	
355 360 365	
TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC	1152
Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val	
370 375 380	
GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA	1200
Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg	
385 390 395	
GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA	1248
Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln	
400 405 410	
AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG	1296
Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu	
415 420 425 430	
GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT	1344
Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser	
435 440 445	
CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT	1392
Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn	
450 455 460	
GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT	1440
Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe	
465 470 475	
ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA	1488
Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu	
480 485 490	
CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA	1536
Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser	
495 500 505 510	
CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT	1584
Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr	
515 520 525	
GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT	1632
Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn	
530 535 540	
CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA	1680
His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys	

545	550	555	
AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA			1728
Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln			
560	565	570	
GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT			1776
Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu			
575	580	585	590
TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT			1824
Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn			
595	600	605	
ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC			1872
Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile			
610	615	620	
ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG			1920
Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met			
625	630	635	
AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA			1968
Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile			
640	645	650	
TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA			2016
Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala			
655	660	665	670
TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG			2064
Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu			
675	680	685	
ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC			2112
Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val			
690	695	700	
TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG			2160
Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg			
705	710	715	
CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG			2208
Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys			
720	725	730	
TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA			2256
Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser			
735	740	745	750
CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA			2304
Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr			
755	760	765	

AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC	2352
Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe	
770 775 780	
GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC	2400
Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser	
785 790 795	
GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA	2448
Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro	
800 805 810	
CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA	2496
Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly	
815 820 825 830	
AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA	2544
Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu	
835 840 845	
ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC	2592
Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser	
850 855 860	
ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG	2639
Met Asp Thr Ser Asn Lys Glu Glu Lys	
865 870	
TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC	2699
CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC	2759
AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC	2819
AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT TGTCAGCAGAT TGTTTCCTCT	2879
TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG	2939
ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC	2999
TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG	3059
TGTCCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA	3119
ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT	3179
AGATTTTATT TTAATTTATG AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT	3239
TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC	3299
AGATTTTATA CCTCAGAATG TAAAGAACT TACTGATTAT TTTCTTCATC CAAGTTATGT	3359
TTTAAATGA GGATTATTGA TAGT	3383

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala
1				5					10					15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp
			20					25					30		
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu
			35					40				45			
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu
	50						55				60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys
65					70				75					80	
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys
				85					90					95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu
			100					105					110		
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val
		115					120					125			
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val
	130					135				140					
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala
145					150					155				160	
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln
			165						170					175	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys
			180					185					190		
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met
		195					200					205			
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp
	210					215				220					

Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235	240
Thr	Gly	Ser	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	245	250	255	
Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	260	265	270	
Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	275	280	285	
Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	290	295	300	
Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	305	310	315	320
Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	325	330	335	
Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	340	345	350	
Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	355	360	365	
Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	370	375	380	
Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	385	390	395	400
Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	405	410	415	
Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	420	425	430	
Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	435	440	445	
Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	450	455	460	
Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	465	470	475	480
Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	485	490	495	
Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	500	505	510	

Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	515	520	525
Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	530	535	540
Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	545	550	555
Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	565	570	575
Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	580	585	590
Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	595	600	605
Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	610	615	620
Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	625	630	635
Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	645	650	655
Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	660	665	670
Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	675	680	685
Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	690	695	700
Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	705	710	715
Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	725	730	735
Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	740	745	750
Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	755	760	765
Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	770	775	780
Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	785	790	795

Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys
805 810 815

Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys
820 825 830

His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr
835 840 845

Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp
850 855 860

Thr Ser Asn Lys Glu Glu Lys
865 870

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	

AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GGT GAT ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Gly Asp Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
240 245 250	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
255 260 265 270	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
275 280 285	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
290 295 300	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	

305	310	315	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg 320 325 330			1008
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser 335 340 345 350			1056
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val 355 360 365			1104
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile 370 375 380			1152
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu 385 390 395			1200
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser 400 405 410			1248
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe 415 420 425 430			1296
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr 435 440 445			1344
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys 450 455 460			1392
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn 465 470 475			1440
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val 480 485 490			1488
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr 495 500 505 510			1536
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe 515 520 525			1584

GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
530 535 540	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
545 550 555	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
560 565 570	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
575 580 585 590	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
595 600 605	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
610 615 620	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	

735	740	745	750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA				2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr				
755		760	765	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA				2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile				
770	775		780	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG				2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg				
785	790		795	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA				2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys				
800	805		810	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA				2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg				
815	820	825	830	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG				2544
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln				
835	840		845	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT				2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser				
850	855		860	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT				2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp				
865	870		875	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG				2688
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu				
880	885		890	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA				2736
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg				
895	900	905	910	
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA				2784
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu				
915	920		925	
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG				2840
Glu Lys				
TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC				2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC				2960

ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTCAGAT GTTTCCTCT TCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3200
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA	3260
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3320
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3380
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3440
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT	3500
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3554

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	
1				5					10					15	
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp
			20					25					30		
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu
		35					40					45			
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu
		50				55					60				
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys
65				70					75					80	
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys
			85					90						95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Gly	Asp
		100					105						110		
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val

115						120						125			
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val
130						135						140			
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala
145					150					155					160
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln
				165					170					175	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys
			180					185					190		
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met
	195						200					205			
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp
210						215				220					
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys
225					230					235					240
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly
				245					250					255	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg
			260					265					270		
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val
		275					280					285			
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly
	290					295					300				
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg
305					310					315					320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe
			325						330					335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu
		340						345					350		
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val
	355						360					365			
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln
	370					375					380				
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu
385					390					395					400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu

405	410	415
Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys		
420	425	430
Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu		
435	440	445
Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu		
450	455	460
Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn		
465	470	475
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala		
485	490	495
Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu		
500	505	510
Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe		
515	520	525
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg		
530	535	540
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser		
545	550	555
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser		
565	570	575
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu		
580	585	590
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser		
595	600	605
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser		
610	615	620
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys		
625	630	635
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg		
645	650	655
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu		
660	665	670
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu		
675	680	685
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met		

690

695

700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
915 920 925